Remarks

Claims 37-41 are pending and currently under examination. Claims 1, 9-12, 24, 25, 28, 29, 42, and 43 are pending and withdrawn from consideration. Claims 2-8, 13-23, 26, 27, and 30-36 have been canceled without prejudice. Certain of the claims have been amended for the purpose of expediting the patent application process in a manner consistent with the Patent and Trademark Office Patent Business Goals (PBG), 65 Fed. Reg. 54603 (September 8, 2000), advance prosecution, and facilitate the business interests of Applicants. Support for the present amendments can be found throughout the specification and claims as filed. For example, support for amended claims 37 and 41 can be found at page 347, lines 1-3, and at page 348, lines 24-27 of the originally filed specification. The undersigned respectfully submits that no new matter has been added. Favorable consideration of the claims now presented, in view of the remarks and amendments set forth herein, is earnestly solicited.

The Office Action of October 22, 2002 included a Notice of Draftsperson's Review that required revisions to several of the drawings filed with this application. Corrected Figures have been submitted to the Patent Office on this same date under separate cover via the U.S. Postal Service.

In the Office Action dated October 22, 2002, claims 37-41 were rejected under 35 U.S.C. § 101 for lacking specific, substantial and well established utility. The polypeptides of the claims are disclosed in the specification as (i) members of the glycerophosphodiester phosphodiesterase family; and (ii) proteins that interact with RGSs. As such, the polypeptides of claims 37-40 play important roles both in lipid metabolism and in G protein signaling.

The Office Action compares the claimed polypeptide with the MIR16 glycerophosphodiester phosphodiesterase (GP-PDE) and indicates that the MIR16 catalytic site is located at amino-acids positions 70-150 of MIR16. The Office Action further notes that amino acids 1-87 of SEQ ID NO:253 are matched with amino acids 1-87 of MIR16, but that amino acids 88-108 of SEQ ID NO:253 are not matched with those of MIR16. Thus SEQ ID NO:253 does not contain the totality of the GP-PDE family catalytic site. The Office Action then asserts that it is not established whether or not SEQ ID NO:253 is a functional GP-PDE and that SEQ ID NO:253 does not possess a substantial, specific, and/or well established utility. The Office Action further asserts that SEQ ID NO:253 has no substantial utility since it would require basic research to further characterize SEQ ID NO:253 and to reasonably confirm a "real world" context of use. Finally, the Office Action indicates that

since the claimed polypeptides are not supported by either a specific and substantial asserted utility or a well established utility, claims 37-41 are rejected under 35 U.S.C. § 112, first paragraph, on the grounds that one skilled in the art would not know how to use the claimed invention. Applicants respectfully traverse these rejections.

In response to these rejections, Applicants respectfully submit that the claimed invention does have a specific, substantial, and/or well established utility and that one skilled in the art would know how to use the claimed invention. Applicants wish to point out that SEQ ID NO:253 is a splice variant of MIR16, as indicated in paragraph 2, page 346 of the specification. In this paragraph, it is first stated that the cDNA encoding SEQ ID NO:243 only differs from the MIR16 cDNA (AF212862) by extended 5' and 3' termini. Additionally, the encoded proteins are identical, as shown on the alignment attached hereto. It is also respectfully submitted that the cDNA encoding SEQ ID NO:253 differs from the cDNA encoding SEQ ID NO:243 by alternative splicing events. Thus, Applicants respectfully submit that SEQ ID NO:253 is not a novel member of glycerophosphodiester phosphodiesterase family to which MIR16 belongs, rather it is a novel splice variant of MIR16. As shown on the alignment attached hereto, the 87 N-terminal amino-acids of SEQ ID NO:253 are identical to the 87 N-terminal amino-acids of MIR16. Applicants also respectfully submit that splice variants are rarely involved in different biological pathways. In the case of proteins involved in protein-protein interactions, different splice variants rarely interact with unrelated binding partners. Often, they either display different binding affinities for the same binding partners, or interact with related partners that are members of the same family.

Applicants emphasize that it is well established that MIR16 interacts with (binds to) Regulators of G Protein Signaling (RGSs). For example, it is stated at page 4001, column 1, lines 63-65 of Zheng et al. (Proc. Nat. Acad. Sci. 97:3999-4004. (2000)):

We found that MIR16 interacted with full-length RGS16 and RGS_{1-62} and, less strongly, with RGS2, GAIP, and Ret-RGS1 (...).

Accordingly, Applicants respectfully submit that because SEQ ID NO: 253 is a splice variant of a protein interacting with RGSs, one skilled in the art would reasonably conclude that SEQ ID NO:253 interacts with RGSs. In view of such recognition, it is respectfully submitted that the subject invention has utilities that would be recognized by one skilled in the relevant art and that one skilled in the art would know how to use the invention as claimed. For example, the polypeptide of

SEQ ID NO: 253 can be used to detect (bind to) RGSs (such as RGS16) in various assays (e.g., qualitative or quantitative assays). Thus, the polypeptide of SEQ ID NO: 253 can be used to detect RGS16, or other related RGSs as disclosed in Zheng et al., that are expressed by transformed host cells.

Yet another disclosed, readily apparent, and well-known use for the polypeptide of SEQ ID NO: 253 is in the preparation of polyclonal or monoclonal antibodies that can then be used for the detection or isolation of SEQ ID NO: 253 or related polypeptides (see, for example, specification, pages 70-75). As the Office Action points out, and as evidenced by the sequence alignment attached hereto, the 87 N-terminal amino-acids of SEQ ID NO: 253 are identical to the 87 N-terminal amino-acids of MIR16. Accordingly, one skilled in the relevant art would reasonably expect that antibodies prepared against the claimed polypeptide (SEQ ID NO: 253) would not only bind to SEQ ID NO: 253, but such antibodies would also bind to related polypeptides, such as MIR16. Accordingly, one skilled in the art would recognize that antibodies raised against the polypeptide of SEQ ID NO: 253 would have utility in the detection or isolation of GP-PDEs, such as MIR16 (in, or from, transformed host cell expression systems).

In view of the foregoing arguments, Applicants respectfully submit that SEQ ID NO:253 and the polypeptides of amended claims 37-41 have a specific, credible and substantial utility. Consequently, the polypeptides of amended claims 37-41 clearly satisfy the utility requirement under 35 U.S.C. § 101 and that one skilled in the art would know how to use the polypeptides of the claimed invention. Accordingly, Applicants request (i) the standing rejection under 35 U.S.C. § 101; and (ii) the standing rejection under 35.USC112, first paragraph, based on the rejection under 35 U.S.C. § 101, be withdrawn.

The Office Action has also rejected claims 38-41 under 35 U.S.C. § 112, second paragraph, as being indefinite because these claims are dependent from canceled claims. This rejection has been obviated by the present amendment to claims 38-41. Accordingly, reconsideration and withdrawal of the rejection under 35 U.S.C. § 112, second paragraph, is respectfully requested.

In view of the foregoing remarks and the amendments to the claims, Applicants believe that the pending claims are now in condition for allowance, and such action is respectfully requested. The Commissioner is hereby authorized to charge any fees under 37 C.F.R. §§ 1.16 or 1.17 as required by this paper to Deposit Account No. 19-0065.

Applicants also invite the Examiner to call the undersigned if clarification is needed on any of this response, or if the Examiner believes a telephone interview would expedite the prosecution of the subject application to completion.

Respectfully submitted,

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FCE/jaj

Attachments: Marked-Up Version of Amended Claims
Sequence Alignment

MARKED-UP VERSION OF AMENDED CLAIMS

38. (Once Amended) The polypeptide of Claim 37 ~~30~~, wherein said polypeptide comprises an amino acid sequence of a full-length polypeptide sequence of SEQ ID NO: 253.

39. (Once Amended) The polypeptide of Claim 37 ~~30~~, wherein said polypeptide consists of an amino acid sequence of a mature polypeptide sequence of SEQ ID NO: 253.

40. (Once Amended) The polypeptide of Claim 38 ~~31~~, wherein said polypeptide consists of an amino acid sequence of a full-length polypeptide sequence of SEQ ID NO: 253.

42. (Once Amended) A method of producing the polypeptide of Claim 37 ~~30~~, comprising the steps of:

(i) culturing a host cell capable of expressing said polypeptide under conditions suitable for producing said polypeptide; and

(ii) isolating and purifying said polypeptide produced by said host cell.

43. (Once Amended) A method of producing the polypeptide of Claim 41 ~~34~~, comprising the steps of:

(i) culturing a host cell capable of expressing said polypeptide under conditions suitable for producing said polypeptide; and

(ii) isolating and purifying said polypeptide produced by said host cell.

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MIR16                MMLWEDQGGLLGPFSFLLLVLLLVTRSPVNACLLTGSLPVLLRVFSPEPVPSCRALQVLK 60
SEQ ID NO:243        MMLWEDQGGLLGPFSFLLLVLLLVTRSPVNACLLTGSLPVLLRVFSPEPVPSCRALQVLK 60
SEQ ID NO:253        MMLWEDQGGLLGPFSFLLLVLLLVTRSPVNACLLTGSLPVLLRVFSPEPVPSCRALQVLK 60

MIR16                PRDRISAIAHRGGSHDAPENTLAAIRQAAKNGATGVELDIEFTSDGIPVLMHDNTVDRTT 120
SEQ ID NO:243        PRDRISAIAHRGGSHDAPENTLAAIRQAAKNGATGVELDIEFTSDGIPVLMHDNTVDRTT 120
SEQ ID NO:253        PRDRISAIAHRGGSHDAPENTLAAIRQLRME-QQAWSWTLSLLLTGFLS----------- 108

MIR16                DGTGRLCDLTFEQIRKLNPAANHRLRNDFPDEKIPTLREAVAECLNHNLTIFFDVKGHAH 180
SEQ ID NO:243        DGTGRLCDLTFEQIRKLNPAANHRLRNDFPDEKIPTLREAVAECLNHNLTIFFDVKGHAH 180
SEQ ID NO:253        ------------------------------------------------------------

MIR16                KATEALKKMYMEFPQLYNNSVVCSFLPEVIYKMRQTDRDVITALTHRPWSLSHTGDGKPR 240
SEQ ID NO:243        KATEALKKMYMEFPQLYNNSVVCSFLPEVIYKMRQTDRDVITALTHRPWSLSHTGDGKPR 240
SEQ ID NO:253        ------------------------------------------------------------

MIR16                YDTFWKHFIFVMMDILLDWSMHNILWYLCGISAFLMQKDFVSPAYLKKWSAKGIQVVGWT 300
SEQ ID NO:243        YDTFWKHFIFVMMDILLDWSMHNILWYLCGISAFLMQKDFVSPAYLKKWSAKGIQVVGWT 300
SEQ ID NO:253        ------------------------------------------------------------

MIR16                VNTFDEKSYYESHLGSSYITDSMVEDCEPHF 331
SEQ ID NO:243        VNTFDEKSYYESHLGSSYITDSMVEDCEPHF 331
SEQ ID NO:253        --------------------------------
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